

CLUSTAL 2.0.12 multiple sequence alignment

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SIN2      -----
SIN4      MRGGASSGPQRWGSAGTTPRSLSTGSSPRGSDD--RSSDDGEELVEVTLDDLQDDDTIVLR 58
SIN6      MRGLPGHERR-WTSDTVSSDKDFSGELSPGADSGYNSGFASEEFVEVTLDDLQDDDTIILR 59
SIN8      MRGLPGHERR-WTSDTVSSGKDLSCGESSPGTDSGNISGFASEEFVEVILDDLQDDDTIILR 59
SIN10     MRGLPGHERR-WTSDTVSSGKDLSCGESSPGTDSGNISGFASEEFVEVILDDLQDDDTIILR 59
SIN12     MKPFSKNDRRRWSFDSVSAGKTAVGSASTSPGT-EYSINGDQEFVEVTIDLQDDDTIVLR 59
SIN14     -----MKMRRGNSSNDHELGLRGANSDTNSDTESIASDRGAFSGPLGRP--KR 47
SIN16     -----MQ--NSENHHPH-----HQHHHSDTEIIGNDRASYSGPLSGPLNKR 39
SIN18     -----
SIN20     -----MSRVSFVVS-----GGYHSDAEAGNS--GPMSGGQLPPIYKK 35
SIN22     -----MMNRSEMQLGFEHVRYT--ESPNRG 26

SIN2      -----
SIN4      SVEPAAAAAAG-----VGAGAGAASARGELTCGPSSSSSSSRSPSIRRSS-SHRLQLQFSQ 112
SIN6      SVEPATVINIDAPDLPAGVGISGVSIIE---TPTSAS-VSESRSPTIIRSS-SSKLRQFSQ 114
SIN8      SVEPATVINIDASDPATGVGIGVSIIE---TPASLTSTSGTRSPMTMRRST-SNKLRLQFSQ 115
SIN10     SVEPATVINIDGSDPASGVGIGGASIE---TPASVTSTSETRSPMMRRST-SNKFRQFSQ 115
SIN12     SVEPATAINV-----IGDISDD---NTGIMTPVSISRSPMTMKRTS-SNRFRLQFSQ 105
SIN14     ASKKNARF--ADDLPKRSNSVAGGRGD---DDEYVEITLDIRDDSVAVHS-VQQAAGGGG 101
SIN16     GGKKSARFNIPSTDIGTSVGTGCKSN---DDAYVEITLDVREDSVAVHS-VKTAGG--D 93
SIN18     -----MASPYDHQSPHAQHPSGLPRPPGAGA 26
SIN20     PG--NSRF-----TAENSQRTR--TAPYVDLTVDVQDDTVSVHS-LKMEGGS-S 78
SIN22     ESSANVAT-----TSNYYGE---DEPYVEITLDIHDDSVSVYG-LKSPNHRGA 70

SIN2      -----
SIN4      ELKAEAMARARQFSQDLT---KRFRSH-----SRSEAPSPG-LESAL--A 153
SIN6      ELKAEAVAKARQFSQELKAEELRRFWSHGHASRAFSPSSFFQNAVVGTTGNG-VDSAL--A 171
SIN8      ELKAEAVAKAKHFSQELKAEELRRFWSHGHASRTFSPASFFQNAVVGTTGNG-VDSAL--A 172
SIN10     ELKAEAVAKAKHFSQELKAEELRRFWSHGHASRAFSPASFFQNAVVGTTGNG-VDSAL--A 172
SIN12     ELKAEAVAKAKQLSQELK---RFSWSRSFSG-NLTTTSTAANQSCGAGGLVNSAL--E 158
SIN14     HLEDPELALLTKKTLESSLNNTTSLSFERS-----TSSRIKNASRELRRVF--S 148
SIN16     DVEDPELALLAKG-LEK--KSTLGSSLVRN-----ASSRIRQVSQELRRLA--S 137
SIN18     GAAAGGFARGLMKQPSR-----LASGVRQFASRVSMKVPEG 62
SIN20     VEESPELTLLKRNRIEK---KTTVVKRLAS-----VSHELKRLTSVSGGIG--G 122
SIN22     GSNYEDQSLLRQGRSGR--SNSVLKRLASS-----VSTGITRVASSVSSSS--A 115

SIN2      -----
SIN4      ARAARRQRAQLDRTRSGAHKALRGLRFISSNKA--NNAWMEVQANFDRLAR--DGYLSRSD 210
SIN6      ARALRRQRAQLDRTRSSAHRALRRLKFISSNK--TNGWNEVENNFASKLAK--DGYLYRSD 227
SIN8      ARALRRQRAQLDRTRSSAHKALRGLKFISSNK--TNGWNEVENNFASKLAK--DGYLYRSD 228
SIN10     ARALRRQRAQLDRTRSSAHKALRGLKFISSNK--TNGWNEVENNFASKLAK--DGYLYRSD 228
SIN12     ARALRRQRAQLDRTRSSAQRALRGLRFISNKQKNVDGWNVDVQSNFEKFEK--NGYIYRSD 216
SIN14     RRPSPAVR-RFDRTSSAAIHALKGLKFIATKT--AAWPAVDQRFDKLSADSNGLLSAK 204
SIN16     LNKRPPIPTGRFDRNKSAAAHALKGLKFIKTDG-GAGWAAVEKRFDEITASTTGLLPRAK 196
SIN18     VGGMRPGGGRMTRMQSSAQVGLRGLRFLDKTSGGKEGWKSVERRFDEMNR--NGRLPKES 120
SIN20     RK--PPRPAKLDRTKSAASQALKGLKFIKTDG-GAGWSAVEKRFNQITATTGGLLLRTK 179
SIN22     RKPPRPQLAKLRRSKSRAELALKGLKFIKTDG-VTGWPEVEKRFYVMTMTNNGLLHRSR 174

SE07D NO:25

SIN2      -----
SIN4      FAECIG-----MTESKEFALELFDLTLRRLRQMK-VDTIN 243
SIN6      FAQCIG-----MKDSKEFALELFDALSRRRLK-VDKIS 260
SIN8      FAQCIG-----MKDSKEFALELFDALSRRRLK-VDKIS 261
SIN10     FAQCIGQYSRRRSIQFNYRLITLILINYLVKGMKDSKEFALELFDALSRRRLK-VDKIS 287

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SIN12	FAQCIG-----	-----MKDSKEFALELFDALSRRRLK-VEKIN	249
SIN14	FWECLG-----	-----MNKESKDFADQLFRALARRNNVS-GDAIT	238
SIN16	FGECIG-----	-----MNKESKEFAVELYDALARRRNIT-TDSIN	230
SIN18	FGKCIG-----	-----MGDSKEFAGELFVALARRRNLEPEDGIT	154
SIN20	FGECIG-----	-----MT--SKDFALELFDALARRRNIT-GEVID	211
SIN22	FGECIG-----	-----MK--STEFALALFDALARRENVS-GDSIN	206

SIN2	-----	-----	
SIN4	KDELREIWQQITDNSFDSRLQIFFEMVDKNADGRITEAEVKEIIMLSASANKLSRLKEQA	303	
SIN6	KEELYEYWSQITDQSFD SRLQISFDMVDKNEDGRIAEEEEVKEIIMLSASANKLSRLKEQA	320	
SIN8	KEELYEYWSQITDQSFD SRLQIFFDMVDKNEDGRIGEEEEVKEIIMLSASANKLSRLKEQA	321	
SIN10	QEELYEYWSQITDQSFD SRLQIFFDMVDKNEDGRIGEEEEVKEIIMLSASANKLSRLKEQA	347	
SIN12	HDELYEYWSQINDESFD SRLQIFFDIVDKNEDGRITEEEVKEIIMLSASANKLSRLKEQA	309	
SIN14	KEQLRIFWEQISDESFD AKLQVFFDMVDKDEDGRVTEEEVAEIISLSASANKLSNIQKQA	298	
SIN16	KAQLKEFWDOVADQSFD SRLQTFDDMVDKADAGRITEEEVREIIGLSASANRLSTIQKQA	290	
SIN18	KEQLKEFWEEMTDQNFDSRLRIFFDMCDKNGDGMLTEDEVKEVIILSASANKLAKLKGA	214	
SIN20	GDQLKEFWEQINDQSFD SRLKTFFDMVDKADAGRLTEDEVREL-----	254	
SIN22	MNELKEFWKQITDQDFDSRLRTFFAMVDKSDGRLNEAEVREIITLSASANELDNIRRQA	266	

SEQ ID NO: 26 SEQ ID NO: 27

SIN2	-----	-----	
SIN4	EEYAALIMEELDPEGLGYIELWQLETLLLLQK--DTYMNYSQALSQALSQNLQGLRKK	361	
SIN6	EEYAALIMEELDPERLGYIELWQLETLLLLQK--DTYLNYSQALSQALSQNLHGLRKK	378	
SIN8	EEYAALIMEELDPERLGYIELWQLETLLLLQK--DTYLNYSQALSQALSQNLQGLRKR	379	
SIN10	EEYAALIMEELDPERLGYIELWQLETLLLLQK--DTYLNYSQALSQALSQNLQGLRKR	405	
SIN12	EEYAALIMEELDPERLGYIELWQLETLLLLQK--DTYLNYSQALSQALSQNLQGLRKG	367	
SIN14	KEYAALIMEELDPDNAGFIMIENLEMLLLQAPNQSVRMG--DSRILSQMLSQKLRPAKES	356	
SIN16	DEYAAMIMEELDPNNLGYIMIENLEMLLLQAPNQSVQGG--ESRNLSQMLSQKLRKHTQER	349	
SIN18	ATYASLIMEELDPDDRGYIEIWQLETLLRGM--VSAQAAPKMKRTTSSLARTMIPSRYR	272	
SIN20	-----ESLETLLLLQAATQSVITSTGERKNLSHMMSQRLKPTFNR	293	
SIN22	DEYAALIMEELDPYHYGYIMIENLEILLLLQAPMQDVRDG--ESKKLSKMLSQNLMPQSR	324	

SEQ ID NO: 28

SIN2	-----	-----	
SIN4	SSIRKISTSLSYFFEDNWKRLWLVLALWIGIMAGLFTWKFMQYRNRYVFDVMGYCVTTAKG	421	
SIN6	SPIKRMSTKLVSLOQENWKRIWVLTLWILIMIGLFLWKIFYQYKNKSAFRVMGYCLVTAKG	438	
SIN8	SPIRRMSTKLVSLOQENWKRIWVLVLWILIMIGLFLWKIFYLYKQKSAFQVMGYCLLTAKG	439	
SIN10	SPIRRMSTKLVSLOQENWKRIWVLVLWILIMIGLFLWKIFYQYKQKSAFQVMGYCLLTAKG	465	
SIN12	SRIHRMSSDFVYIMQENWKRIWVLVLWIMIMIGLFLWKFFQYKQKDAFHVGMGYCLLTAKG	427	
SIN14	NPLLRWSEKIKYFILDNWQRLWIMMLWLIGCGGLFTYKFIQYKNKAAYGVMGYCVCVAKG	416	
SIN16	NPIVRWYKSFMYFLLDNWQRVWVLLWIGIMAGLFTWKYIQYKEKAAYKVMGPCVCVFAKG	409	
SIN18	SPLKRHVSRVDFVHENWKRIWLVALWLAVNVGLFAYKFEQYERRAAFQVMGHCVCVAKG	332	
SIN20	NPLKRWYRGLRFFLLDNWQRCWVIVLWFIVMAILFTYKFIQYRRSPVYPVMGDCVCMAKG	353	
SIN22	NLGARFCRGMKYFLFDNWKRVMWVWALWIGAMAGLFTWKFMQYRKRSAAYEVMGVCVCIAKG	384	

SIN2	-----	-----	
SIN4	AAETLKLNMALILLPVCNRTITWLR-STRAARALPFDDNINFHKTIAAAIVVGIILHAGN	480	
SIN6	AAETLKFNMALILLPVCNRTITWLR-STKLSHFVPFDDNINFHKTVAIAIVTGIILHAGN	497	
SIN8	AAETLKFNMALILLPVCNRTITFLR-STKLSCFVPFDDNINFHKTVAIAIVTGIILHAGN	498	
SIN10	AAETLKFNMALILLPVCNRTITFLR-STKLSCFVPFDDNINFHKTVAIAIVTGIILHAGN	524	
SIN12	AAETLKFNMALILFPVCNRTITWLR-STRLSYFVPFDDNINFHKTIAAGIIVVAVILHIGD	486	
SIN14	GAETLKFNMALILLPVCNRTITWLRNKTKLGTVPFDDSLNFHKVIAASGIVGVVLLHAGA	476	
SIN16	AAETLKLNMALILFPVCNRTITWLRNKTRLGAAPFDDNLFHKKVIAVAIALGVGIHGLS	469	
SIN18	AAEVLKLNMALILLPVCNRTITTLR-STALSHVIPFDDNINFHKKVIAATIAAATAVHTLA	391	
SIN20	AAETVKLNMALILLPVCNRTITWLRNKTRLGRVVPFDDNLFHKKVIAVGIIVGVTMHAGA	413	
SIN22	AAETLKLNMAMILLPVCNRTITWLRTKTKLSAIVPFDDNINFHKKVIAIGISVGVGIHATS	444	

SEQ ID NO: 29

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SIN2 -----
SIN4 HLVCDFPRLIKSSDEKYAP-LGQYFGE- IKPTYFTLVKGVEGITGVIMVVCMIIAFTLAT 538
SIN6 HLVCDFPRLIHADDQDYQSFLSNDFGQ-SKPGYIDLKVGVEGVTGIIMVILMAIAFTLAT 556
SIN8 HLVCDFPKLIHANNTNYQKYLVNDFGP-SQPQYIDLKVGVEGVTGIIMVILMAIAFTLAT 557
SIN10 HLVCDFPKLIHANSTNYQKYLVNDFGP-SQPQYIDLKVGVEGVTGIVMVILMAIAFTLAT 583
SIN12 HLACDFPRIVRATEYDYNRYLFHYFQT-KQPTYFDLVKGPEGITGILMVILMIISFTLAT 545
SIN14 HLTCDFPRLIAADEDITYEP-MEKYFGD-QPTSYWWFVKVEGWTGIVMVVLMIAIAFTLAT 534
SIN16 HLTCDFPRLLNASEEBEYEP-MKYYFGD-QPESYWWFIKVEGVTGIIMVVLMIAIAFTLAT 527
SIN18 HVTCDFPRLINCPSDKFMATLGPNFGY-RQPTYADLLESAPGVTGILMIIIMSFSFTLAT 450
SIN20 HLACDFPRLHATPEAYRP-LRQFFGDEQPKSYWHFVNSVEGITGLVMVLLMAIAFTLAT 472
SIN22 HLACDFPRLIAADEDQYEP-MEKYFGP-QTKRYLDFVQSVEGVTGIGMVVLMTIAFTLAT 502

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SIN2 -----
SIN4 RWFRRSLVK-LPRPFDKLTGFNAFWYSHHLLFIIVYIALIVHGECLYLIHV-WYRRTTW-M 595
SIN6 RWFRRSLIK-LPKPFDRLTGFNAFWYSHHLLVIVYILLIIHGTFLLVHK-WYSKTTW-M 613
SIN8 RWFRRSLIK-FPKPFDRLTGFNAFWYSHHLLIIVYIVLIIHGTFLLVHN-WYSKTTW-M 614
SIN10 RWFRRSLIK-LPKPFDRLTGFNAFWYSHHLLIIVYIVLIIHGTFLLVHN-WYSKTTW-M 640
SIN12 RWFRRNLVK-LPKPFDRLTGFNAFWYSHHLLFVIVYILLILHIGIFLYFAKP-WYVRTTW-M 602
SIN14 PWFRRNKLN-LPNFLKKLTGFNAFWYTHHLLFIIVYALLIVHGKLYLTKI-WYQKTTW-M 591
SIN16 PWFRRNRVS-LPKPFLHKLTXNAFWYSHHLLFVIVYTLFIVHGEKLYITKD-WYKRTDMDV 585
SIN18 HSFRRSVVK-LPSPLHLLAGFNAFWYAHHLLVLAYVLLVHVSFYIFLTRE-WYKKTW-M 507
SIN20 PWFRRGKLNYPGPKLKLASFNAFWYTHHLLFVIVYILLVAHGYYLYLTRD-WHNKTTW-M 530
SIN22 TWFRRNKLN-LPGPLKKITGFNAFWYSHHLLFVIVYSLLVVHGIFYVYLLIEPWyKKTW-M 560

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SIN2 -----
SIN4 YLSVPVCLYVGERILRFFRSGSYSVRLLKVAIYPGNVLTLMQSKPPTFRYKSGQYMFVQC 655
SIN6 YLAVPVLLYAGERTLRFFRSGLYTVRLLKVAIYPGNVLTLMQSKPPQFRYKSGQYMFVQC 673
SIN8 YLAVPVLLYAGERTLRFFRSGLYTVRLLKVAIYPGNVLTLMQSKPPQFRYKSGQYMFVQC 674
SIN10 YLAVPVLLYAGERTLRFFRSGLYSVRLLKVAIYPGNVLTLMQSKPPQFRYKSGQYMFVQC 700
SIN12 YLAVPVLLYGGERTLRYFRSGSYSVRLLKVAIYPGNVLTLMQSKPTQFRYKSGQYMFVQC 662
SIN14 YLAVPILLYASERLLRAFRSSIKPVKMIKVAVYPGNVLSLHMTKPQGFYKSGQYMFVNC 651
SIN16 LLTIPIILYASERLIRAFRSSIKAVKILKVAVYPGNVLSLHMSKPPGFKYKSGQYMFVNC 645
SIN18 YLIVPVLFYACERTIRKVRENNYRVSIVKAAIYPGNVLSLHMKKPPGFKYKSGMYLFFVKC 567
SIN20 YLVVPVLYACERLIRAFRSSIKAVTIRKVAVYPGNVLSLHLSRPQNFYKSGQYMFVNC 590
SIN22 YLMVPVLYLCERLIRAFRSSVEAVSVLKVAVLPGNVLSLHLSRPSNFRYKSGQYMYLNC 620

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SIN2 -----
SIN4 PAVSPFEWHPFSITSAPGDDYLSIHVRQLGDWTRELKRVFAAAACEPPAGGKSG-LLRAD- 713
SIN6 PAVSPFEWHPFSITSAPGDDYLSIHVRQLGDWTQELKRVFSEACERPEAGKSG-LLRAD- 731
SIN8 PAVSPFEWHPFSITSAPGDDYLSIHVRQLGDWTQELKRVFSEACEQPEAGKSG-LLRAD- 732
SIN10 PAVSPFEWHPFSITSAPGDDYLSIHVRQLGDWTQELKRVFSEACEQPEAGKSG-LLRAD- 758
SIN12 PAVSPFEWHPFSITSAPEDDYLSIHVRQLGDWTQELKRVFSEVCEPPVGGKSG-LLRAD- 720
SIN14 RAVSPFEWHPFSITSAPGDDYLSVHIRTLDGWTQELKRVFSEVCKPPTAGKSG-LLRAD- 709
SIN16 AAVSPFEWHPFSITSAPGDDYLSVHIRTLDGWTQELKRVFSEVCKPPPNKGKSG-LLRADY 704
SIN18 PDVSPFEWHPFSITSAPGDDYLSVHIRTLDGWTQELKRVFSEVCKPPPNKGKSG-LLRADY 627
SIN20 AAVSPFEWHPFSITSAPQDDYLSVHIRTLDGWTQELKRVFSEVCKPPPNKGKSG-LLRADY 649
SIN22 SAVSTLEWHPFSITSAPGDDYLSVHIRTLDGWTQELKRVFSEVCKPPPNKGKSG-LLRADY 679

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SEQ ID NO: 30 SEQ ID NO: 31

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SIN2 -----
SIN4 -----ETTKILPKLLIDGPYGSPAQDYKYDVLVLLVGLGIGATPFISILKDLLNIIK 767
SIN6 -----ENTKSLPKLLIDGPYGAPAQDYKYDVLVLLVGLGIGATPFISILKDLLVNIK 785
SIN8 -----ENTKSLPKLLIDGPYGAPAQDYKYDVLVLLVGLGIGATPFISILKDLLKNIVT 786
SIN10 -----ENTKSLPKLLIDGPYGAPAQDYKYDVLVLLVGLGIGATPFISILKDLLKNIVA 812
SIN12 -----ETTKSLPKLLIDGPYGAPAQDYKYDVLVLLVGLGIGATPFISILKDLLNIIK 774
SIN14 -----GGDGNLPPFKVLIDGPYGAPAQDYKYDVLVLLVGLGIGATPMISILKDIINNMKG 764
SIN16 -----LQGENNPNFPRVLIDGPYGAPAQDYKYDVLVLLVGLGIGATPMISIVKDIINNMKA 760

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SIN18 TVVADAQTEDTRFPKVLIDGPYGAPAQNYKKYDILLIGLGIGATPFISILKDLLNNIKS 687
 SIN20 ----LHGANNPDFPKVLIDGPYGAPADYKKYEVVLLVGLGIGATPMISIVKDIVNNIKA 705
 SIN22 ----KHWDYIPDFPRILIDGPYGAPADYKKFEVVLLVGLGIGATPMISIVSDIINNKG 735

SEQ ID NO: 32

SEQ ID NO: 33

SIN2 -----
 SIN4 MEEEEASTDLYPPMGRNKPVDLGLTMTI--TSRPK--KILKTTNAYFYWVTREQGSFDW 824
 SIN6 MEEQADLASDFSGNSDMSVATSEQPALNKISLKRK--STLRTTNAYFYWVTREQGSFDW 843
 SIN8 MEEQADLVSDFSGNSDMSAATSEQPALNKISPKKRK--STLKTTNAYFYWVTREQGSFDW 844
 SIN10 MEEQADLVSDFSGNSDMSAATSEQPALNKISPKKRK--STLKTTNAYFYWVTREQGSFDW 870
 SIN12 MEEHADSISDFRSSEYSTGSNGD-----TPRRK--RILKTTNAYFYWVTREQGSFDW 825
 SIN14 PDRDS----DIENNNNSNNNS-----KG-----FKTRKAYFYWVTREQGSFEW 802
 SIN16 MDEEENSLEDGHNNNNMAPNSSPNIAKNKGNKSGSASGGNNFNTRRAYFYWVTREQGSFDW 820
 SIN18 NEEVESIHGSEIGSFKNNGPG-----RAYFYWVTREQGSFEW 724
 SIN20 KEQAQLN--RMENGTSEPQRS-----KKES-----FRTRRAYFYWVTREQGSFDW 748
 SIN22 VEEGSNRRQSPIHNMVTPPVSPS--RKSE-----TFRTKRAYFYWVTREQGSFDW 783

SEQ ID NO: 34

SIN2 FKGIMNEIAELDQRNIIEMHNYLTSVYEEGDARSALITMLQALNHAKNGVDVVSXTRVRT 60
 SIN4 FKGVMNEIADLDQRNIIEMHNYLTSVYEEGDARSALITMLQALNHAKNGVDIVSGTKVRT 884
 SIN6 FKGVMNEVAELDQRGVIEHNYLTSVYEEGDARSALITMVQALNHAKNGVDIVSGTRVRT 903
 SIN8 FKGVMNEVAELDQRGVIEHNYLTSVYEEGDARSALITMVQALNHAKNGVDIVSGTSVRT 904
 SIN10 FKGVMNEVAELDQRGVIEHNYLTSVYEEGDARSALITMVQALNHAKNGVDIVSGTSVRT 930
 SIN12 FKGVMNEVAELDQRGVIEHNYLTSVYEEGDARSALITMVQALNHAKNGVDIVSGTRVRT 885
 SIN14 FKGIMDEISELDEEGIIELHNYCTSVYEEGDARVALIAMLQSLQHAKNGVDVVSXTRVKS 862
 SIN16 FKGIMNEAAEMDHKGVIEMHNYCTSVYEEGDARSALITMLQSLHAKNGVDIVSGTRVKS 880
 SIN18 FKGVMNDVAESDHNNIIEMHNYLTSVYEEGDARSALIAMVQSLQHAKNGVDIVSGSRIRT 784
 SIN20 FKNIMNEVAERDANRVIEMHNYCTSVYEEGDARSALITHMLQSLNHAKNGVDIVSGTRVMS 808
 SIN22 FKNVMDEVTETDRKIVIELHNYCTSVYEEGDARSALITMLQSLNHAKHGVDVVSXTRVMS 843
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SIN2 HFARPNFKRVLISKVAAKHPYAKIGVFYCGAPVLAQELSNLCHEFNKGKCTTKF----- 112
 SIN4 HFARPNWRKVLISKISSKHPYAKIGVFYCGAPVLAQELSKLCHEFNKGKCTTKFEFHKEHF 943
 SIN6 HFARPNWKKVFSKTLTKHANARIGVFYCGAPVLAQELSKLCHEFNQKGATKFEFHKEHF 962
 SIN8 HFARPNWRKVFSKTLTKHANARIGVFYCGAPILAKELSKLCHEFNQKGTTKFEFHKEHF 963
 SIN10 HFARPNWRKVFSKTLTKHANARIGVFYCGAPILAKELSKLCHEFNQKGTTKFEFHKEHF 989
 SIN12 HFARPNWKKVLTKLSSKHCNARTGVFYCGVPVLGKELSKLCNTFNQKGSTKFEFHKEHF 944
 SIN14 HFAKPNWRQVYKKIAVQHPGKRIGVFYCGMPGMIKELKNLALDFSRKTTTKFDFHKENF 921
 SIN16 HFAKPNWRNVYKRIALNHPEAKVGVFYCGAPALTKELRQHALDFSHKTSTKFDHKENF 939
 SIN18 HFARPNWRKVFSDLANAHKNSRIGVFYCGSPTLTKQLKDLSEKFSQTFTTFRFHKENF 843
 SIN20 HFAKPNWRNVYKRIAMDHPNTKVGVFYCGAPALTKELRHLALDFTHKTSTRFSFKENF 867
 SIN22 HFARPNWRSVFKRIAVNHPKTRVGVFYCGAAGLVKELRHLALDFSHKTSTKFIHKENF 902
 ,:*:: * . * : ** . : : * . . : . . :*:*

SEQ ID NO: 35

Table summarizing the degree of sequence identity between SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 22. The sequence alignment is performed using CLUSTALW program with the default parameters.

SEQ ID NO	2	4	6	8	10	12	14	16	18	20	22
2	-	-	-	-	-	-	-	-	-	-	-
4	89	-	-	-	-	-	-	-	-	-	-
6	79	72	-	-	-	-	-	-	-	-	-
8	78	72	92	-	-	-	-	-	-	-	-
10	78	71	92	98	-	-	-	-	-	-	-
12	76	70	77	77	77	-	-	-	-	-	-
14	66	52	53	52	52	51	-	-	-	-	-
16	66	51	52	51	51	51	67	-	-	-	-
18	64	53	53	53	54	52	49	51	-	-	-
20	64	50	50	50	50	50	61	65	47	-	-
22	62	52	52	52	51	51	59	60	50	62	-